

Figure 1

Patient data

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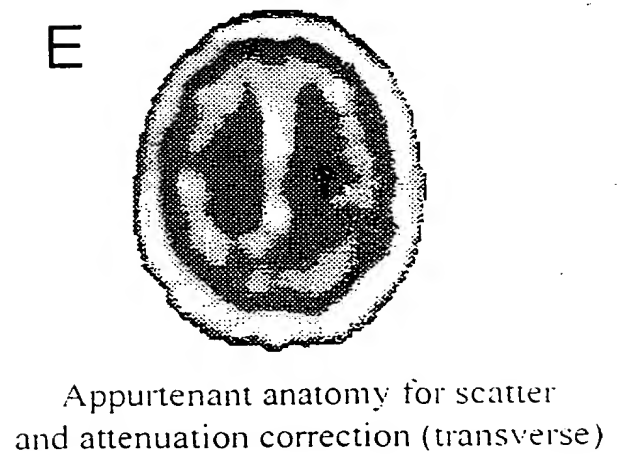
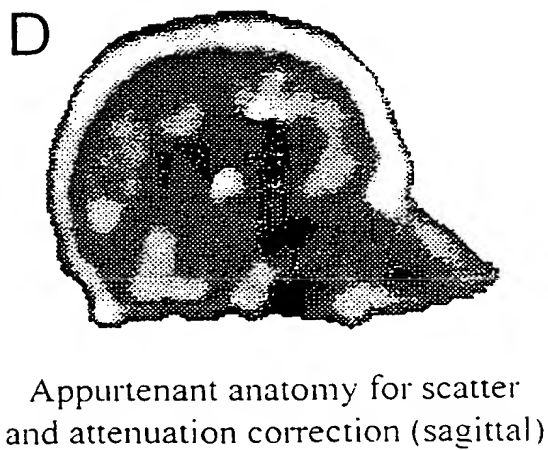
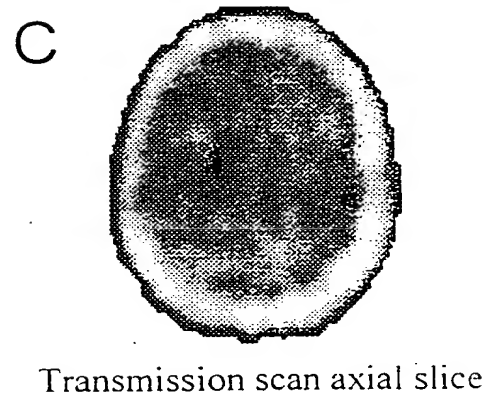
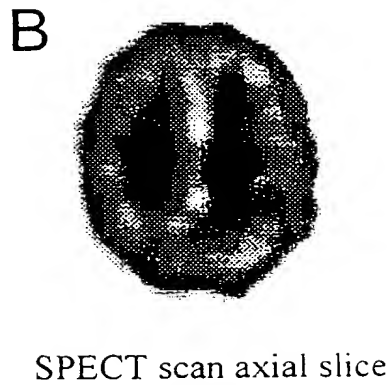
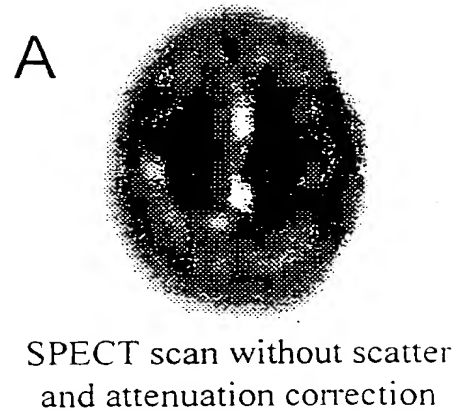
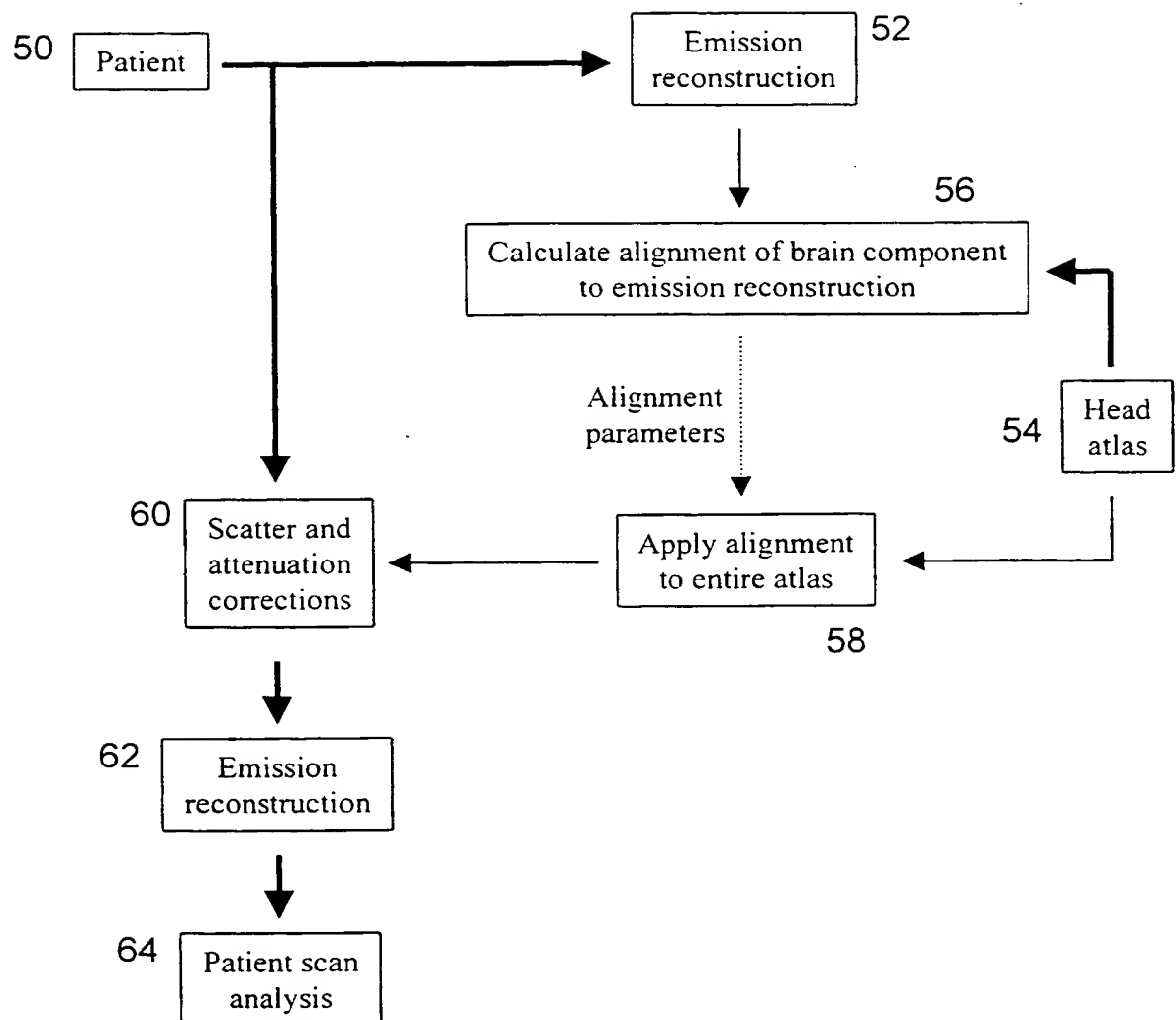


Figure 2

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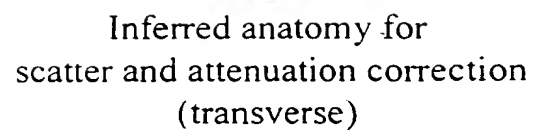
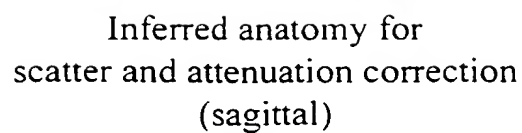
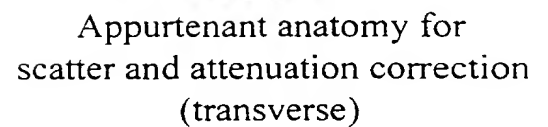
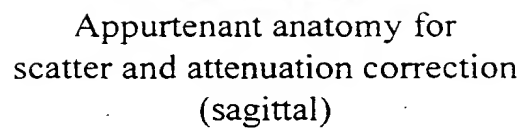
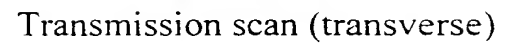
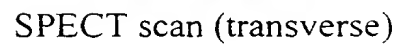
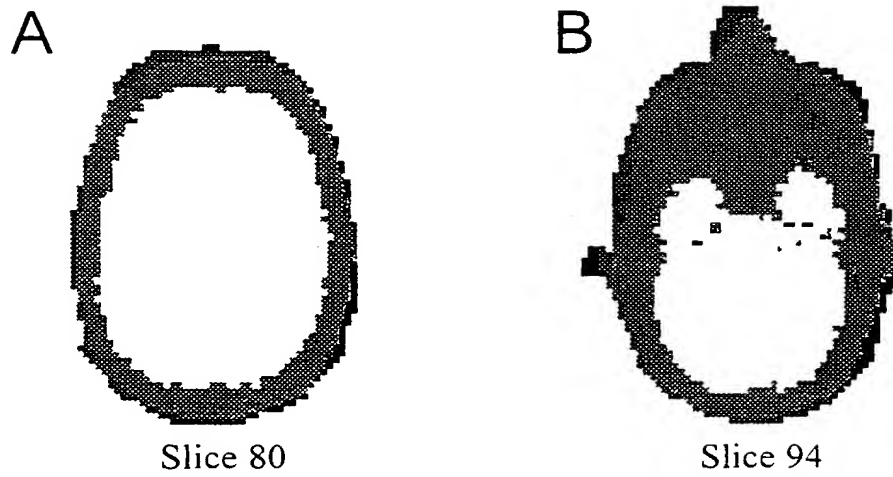
[illegible]

Figure 4

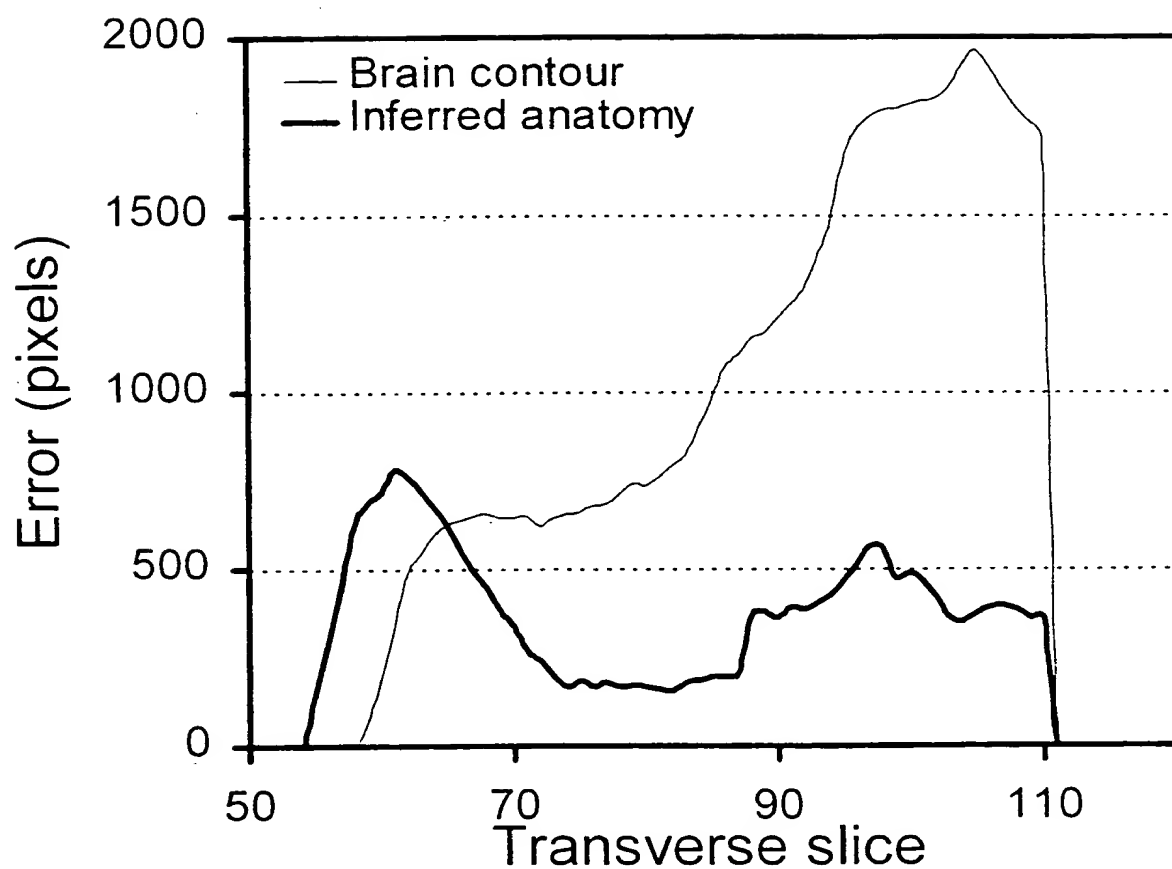
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(A) Mid-cortical and (B) cerebellar transverse slices. Volume enclosed by brain contour (white), appurtenant anatomy (gray), and inferred anatomy (black).

Figure 5

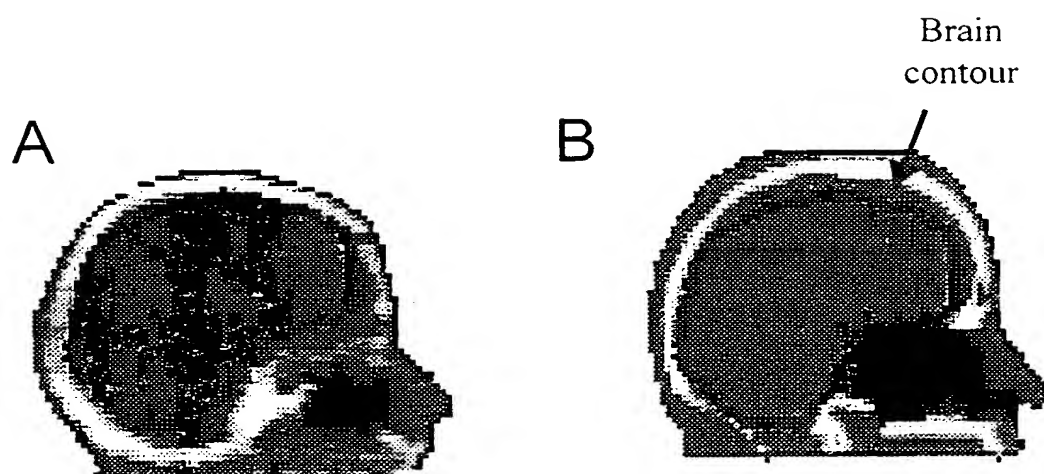
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Both the brain contour and uniform inferred anatomy differ from appurtenant anatomy. Here, this difference (in pixels) is plotted as a function of transverse slice.

Figure 6

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Sagittal slice through (A) appurtenant anatomy and (B) inferred anatomy. The (appurtenant) brain contour is shown as the thick black outline in both (A) and (B).

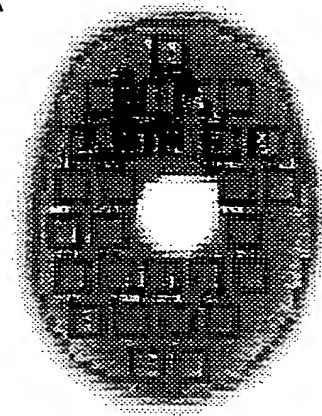
Figure 7

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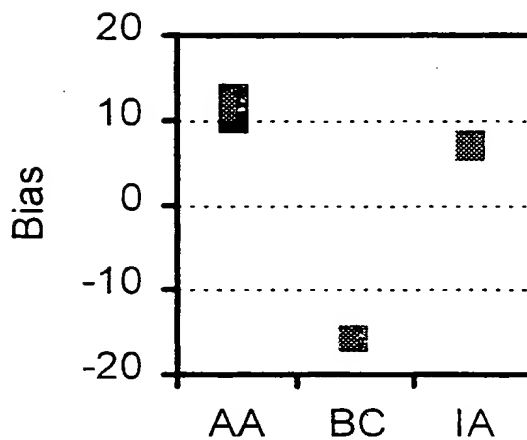
A

SPECT scan of the head phantom. (transverse slice)
Black squares in (A) are a subset of the two-hundred
macrovoxels defined in the reconstructed volume.

The macrovoxels are used in the error metrics
defined below.



B



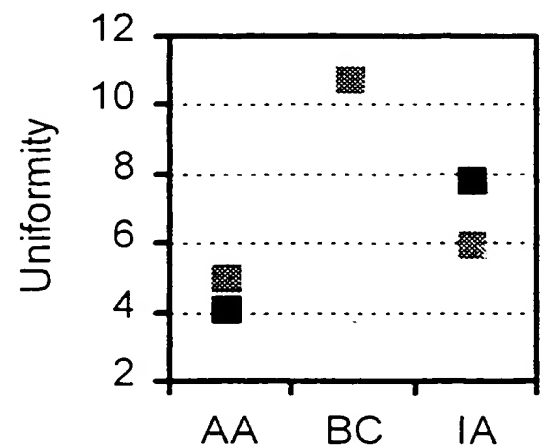
Global bias, shown in (B), was defined as

$$[(\text{mean macrovoxel activity/calibration}) - 1] * 100\%$$

Data is shown for appurtenant anatomy (AA),
braincontour (BC), and inferred anatomy (IA).

Uniform corrections are shown in gray,
and non-uniform in black.

C



Global uniformity, shown in (C), was defined as

$$[(\text{coefficient of variation of macrovoxels}) * 100\%]$$

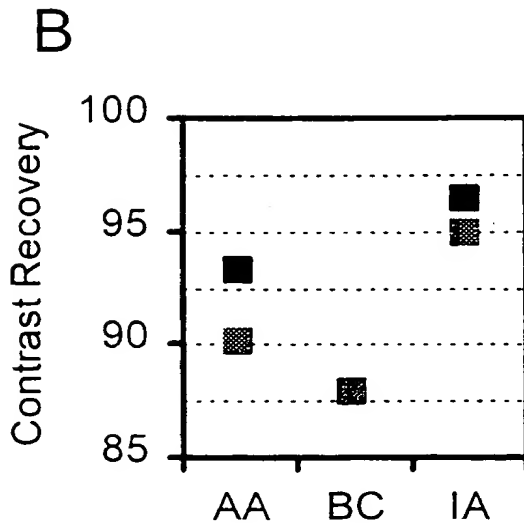
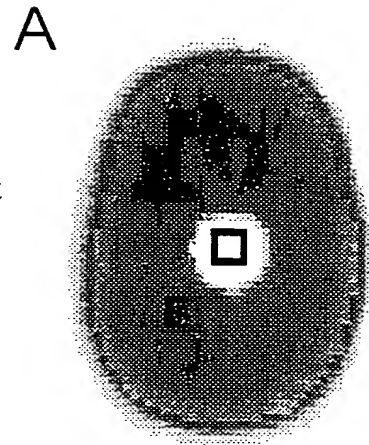
Data is shown for appurtenant anatomy (AA),
braincontour (BC), and inferred anatomy (IA).

Uniform corrections are shown in gray,
and non-uniform in black.

Figure 8

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(A) SPECT scan of phantom (transverse slice at cortical level). Hot and cold regions of interest were defined (hot at centre). The regions were used to calculate contrast recovery and relative quantification, as described in (B) and (C) below.



Contrast recovery (B) was calculated as $[(\text{Hot} / \text{Cold activity}) / \text{true activity ratio}] * 100\%$. Data is shown for appurtenant anatomy (AA), brain contour (BC), and inferred anatomy (IA).

Relative quantification (cortical: cerebellar activity ratio - regions of interest not shown) is presented in (C). Data is shown for appurtenant anatomy (AA), brain contour (BC), and inferred anatomy (IA).

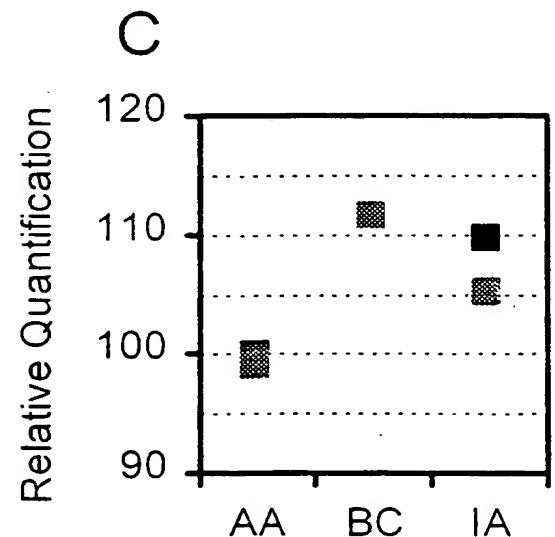
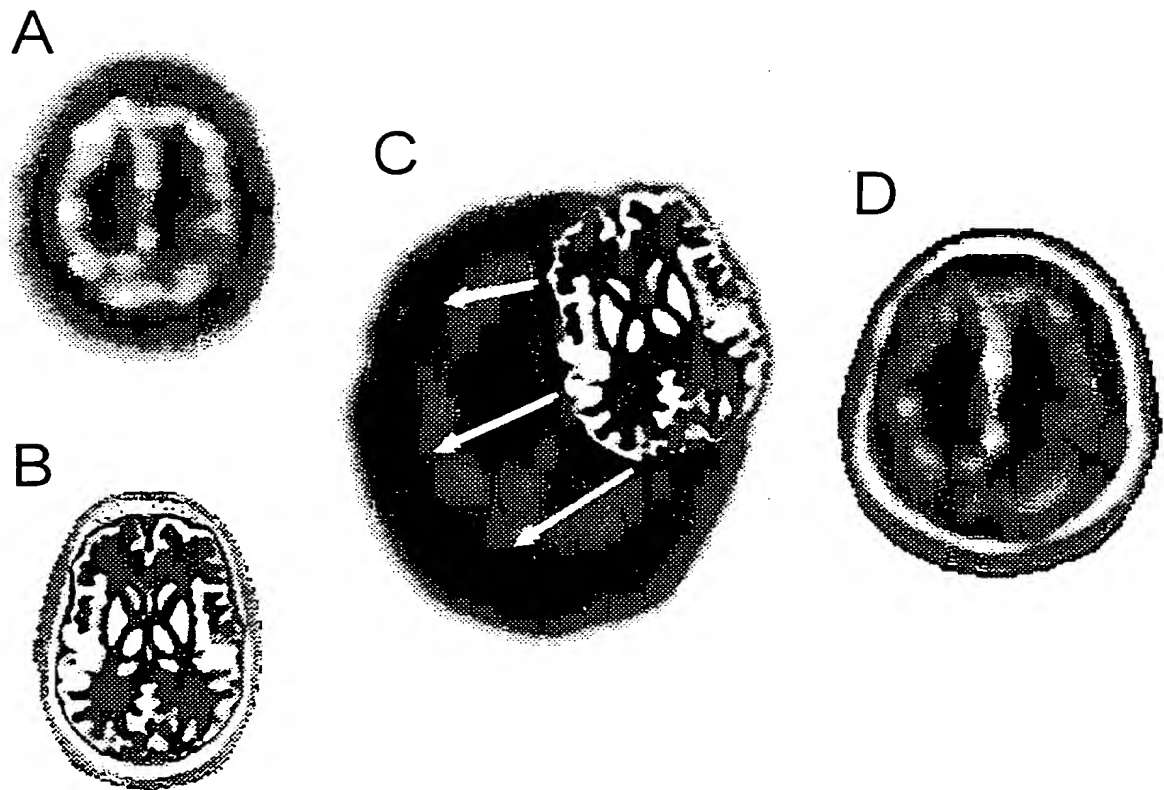


Figure 9

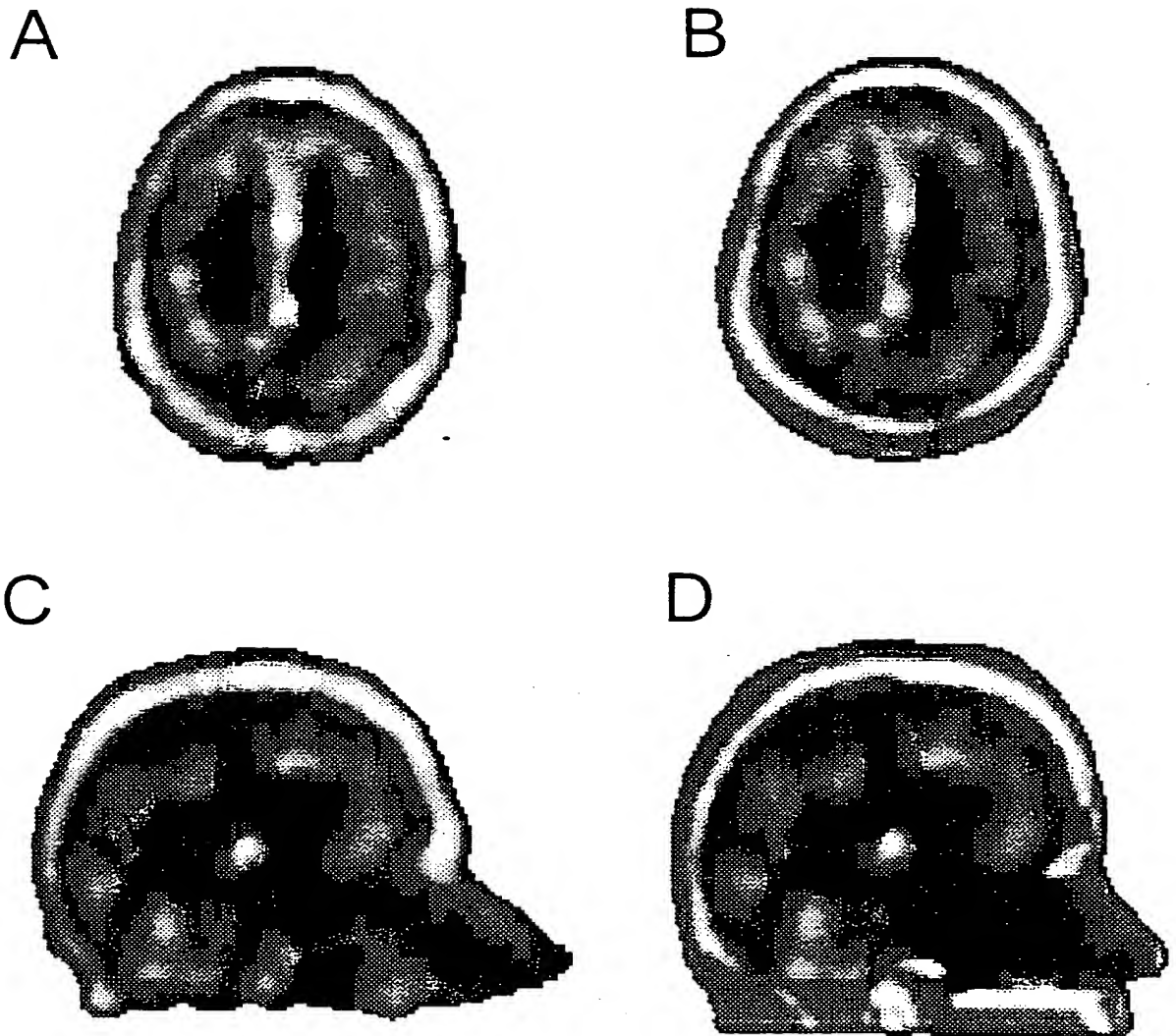
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The Inferred Anatomy algorithm requires a patient's preliminary reconstruction (A) and a head atlas (B). The preliminary reconstruction does not include scatter and attenuation correction. The head atlas consists of a functional component (brain), and an anatomical component (extra-cerebral tissue). The functional component is then spatially registered to the preliminary reconstruction (C), and this optimal transformation is recorded. The patient's anatomy is then inferred by applying the same transformation to the anatomical component of the head atlas (D).

Figure 10

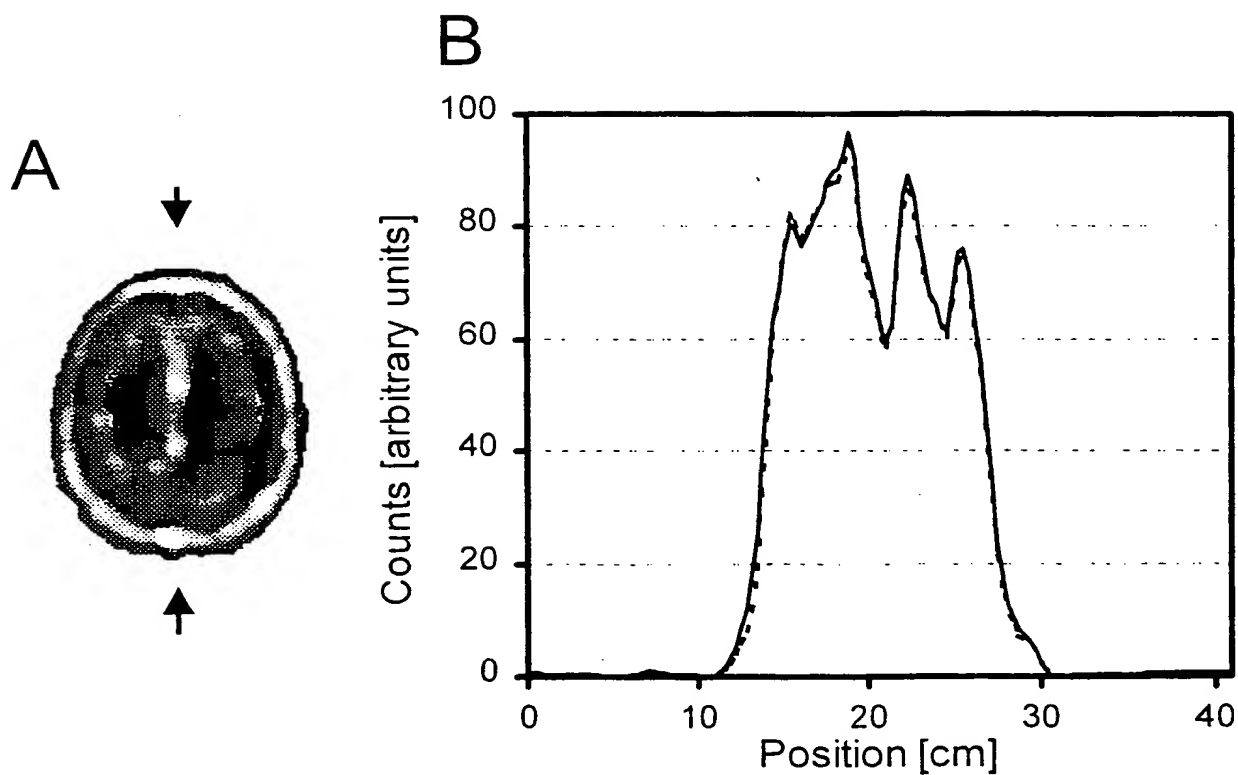
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Examples of a patient's SPECT scan (brain) superimposed onto the pertinent transmission reconstruction (A and C, extra-cerebral tissue) and Inferred Anatomy (B and D, extra-cerebral tissue). The reconstruction includes scatter and attenuation correction guided by either the transmission reconstruction or Inferred Anatomy.

Figure 11

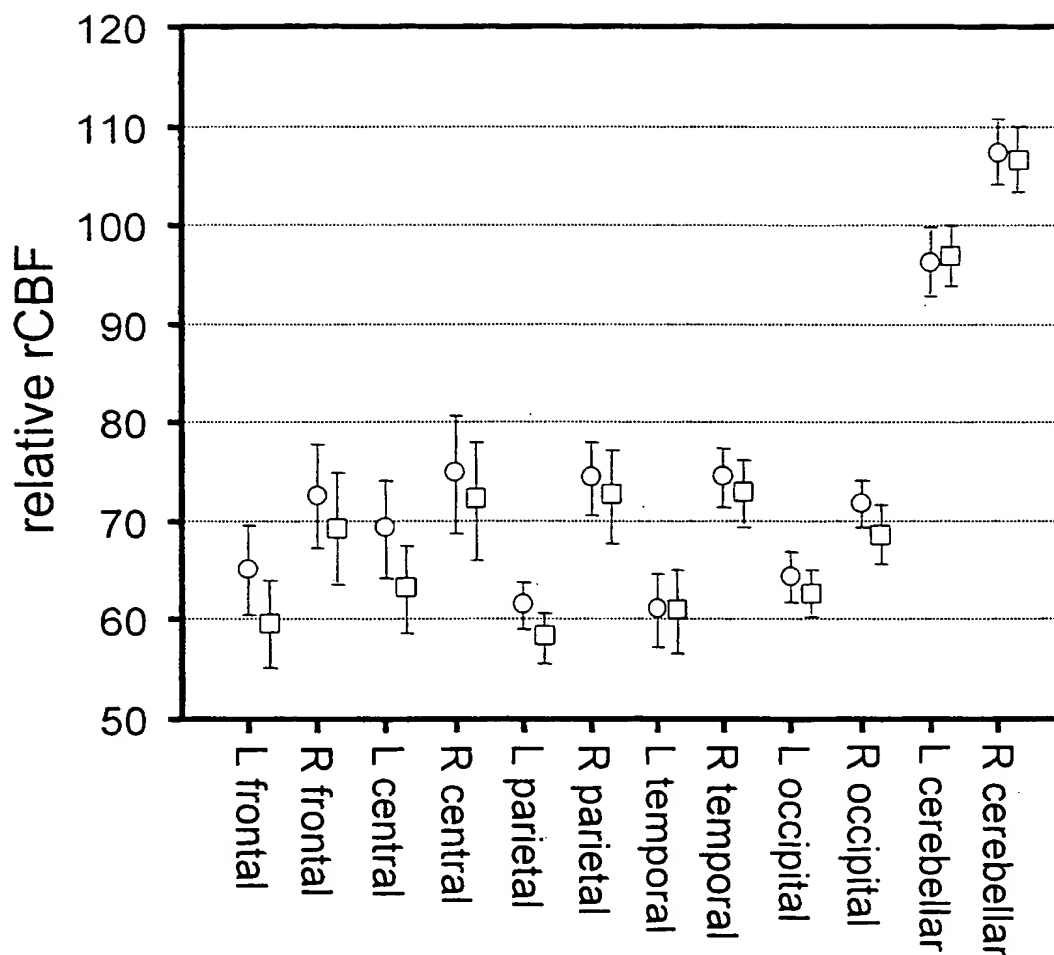
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Profiles (B) through reconstructions at the cortical-axial level (A) comparing a SPECT reconstruction guided by the pertinent transmission scan (solid) with the reconstruction guided by Inferred Anatomy (dots). The profiles were taken between the two arrows in A.

Figure 12

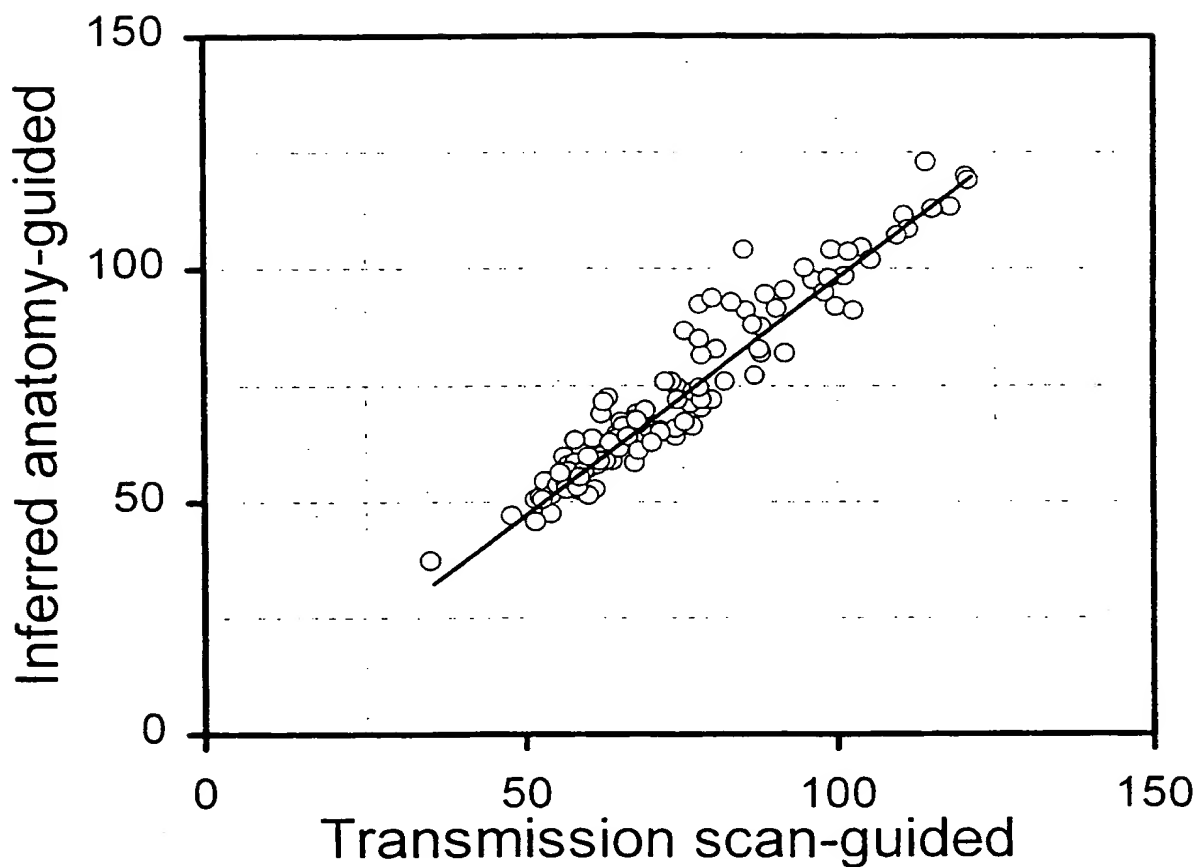
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Regional cerebral blood flow with voxel-by-voxel Lassen's correction, relative to the cerebellum is shown for the twelve bilateral regions-of-interest. Means and standard errors are calculated across the ten patients. The quantification follows scatter and attenuation correction guided by transmission reconstructions (circles) or Inferred Anatomy (squares).

Figure 13

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Comparison of reconstructions guided by transmission scans (abscissa), with reconstructions guided by Inferred Anatomy (ordinate). 120 data points are shown; these are from twelve regions-of-interest and ten patients. Each point represents regional cerebral blood flow with Lassen's correction, relative to the cerebellum. The equation of the line-of-best-fit is $y=1.02x-3.83$, and the correlation coefficient squared is $r^2=0.92$ ($p<<0.0001$).